## IN THE CLAIMS

- 1. (original) An isolated nucleic acid molecule comprising a polynucleotide encoding a phospholipase  $A2\gamma$  polypeptide. (SEQ ID NO:1)
- 2. (original) An isolated nucleic acid molecule in accordance with Claim 1, wherein said phospholipase  $A2\gamma$  polypeptide catalyzes cleavage of fatty acids from the sn-2-position of phospholipids.
- 3. (original) An isolated nucleic acid molecule in accordance with Claim 2 wherein said polynucleotide encodes a sequence as set forth in SEQ ID NO: 1 or SEQ ID NO:2.
- 4. (original) A vector comprising a nucleic acid molecule in accordance with Claim 1.
- 5. (original) A cell transformed or transfected with a vector in accordance with Claim 4.
- 6. (original) An isolated nucleic acid molecule comprising a fragment of a polynucleotide encoding a phospholipase A2 $\gamma$  wherein said fragment specifically hybridizes with a sequence as set forth in at least one of SEQ ID NOS 3, SEQ ID NO:4 and SEQ ID NO:5.
- 7. (original) An isolated nucleic acid comprising a polynucleotide having at least about 90% identity with SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, or SEQ ID NOS 6, 7, 8 or 9 wherein the encoded polypeptide has or modulates enzymatic activity.
- 8. (original) An isolated nucleic acid according to claim 7 comprising SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, or SEQ ID NOS 6, 7, 8 or 9.
- 9. (original) An antisense sequence which specifically hybridizes to SEQ ID NO: 3, or SEQ ID NO: 5 or SEQ ID NO: 6.
  - 10. (original) An isolated polypeptide comprising a phospholipase A2 $\gamma$ .
- 11. (original) An isolated polypeptide in accordance with Claim 10 which catalyzes cleavage of fatty acids from the sn-2-position of phospholipids.

- 12. (original) An isolated polypeptide in accordance with Claim 11 which has at least 90% identity with SEQ ID NO: 1 or SEQ ID NO:2.
- 13. (original) An isolated polypeptide in accordance with Claim 12 comprising SEQ ID NO:1 or SEQ ID NO:2.
- 14. (original) An isolated polypeptide in accordance with Claim 12 which is a conservatively substituted variant of SEQ ID NO:1 or SEQ ID NO:2.
- 15. (original) An antibody capable of binding to a phospholipase  $A_2\gamma$  according to Claim 1.
- 16. (original) A vector comprising a nucleic acid molecule in accordance with Claim 1 suitable for vectoring into a transgenic mouse wherein the reporter gene encodes an enzyme capable of being detected by a colorimetric, fluorometric or luminometric assay.
- 17. (original) A method in accordance with Claim 16 wherein said reporter gene encodes a luciferase.
  - 18-20. (canceled).
- 21. (original) A method for preparing a transgenic mouse which further comprises breeding a transgenic founder mouse having SEQ ID 1 stably integrated in its genome with WT B6CBAE1/J mice.
- 22. (original) A transgenic mouse having in its genome a nucleic acid molecule comprising a polynucleotide encoding a phospholipase A<sub>2</sub>γ polypeptide. (SEQ ID NO: 1)
- 23. (original) A transgenic mouse in accordance with Claim 22 wherein said phospholipase  $A_2\gamma$  polypeptide catalyzes cleavage of fatty acids from the sn-2-position of phospholipids.
- 24. (original) A transgenic mouse in accordance with Claim 23 wherein said polynucleotide encodes a sequence as set forth in SEQ ID NO:1 or SEQ ID NO:2.
  - 25. (canceled).

26. (original) A transgenic mouse having within its genome a nucleic acid molecule comprising a fragment of a polynucleotide encoding a phospholipase  $A_2\gamma$  wherein said fragment specifically hybridizes with a sequence as set forth in SEQ ID NO:3 or SEQ ID NO:4 or SEQ ID NO:5.

## 27-31. (canceled).

- 32. (original) A mitochondrial import signal and cleavage site (LRK/VS) (SEQ ID NO:95) immediately downstream from the 74 kDa alternative start site which directs iPLA<sub>2</sub> $\gamma$  into mitochondria resulting in a truncated protein of approximately 72 kDa.
- 33. (original) A subcellular localization of  $iPLA_2\gamma$  into both peroxisomes and mitochondria which may have important implications for the role of  $iPLA_2\gamma$  in modulating cellular function.
- 34. (original) An alternative exon 5 splice variant utilizing gt/ag splice junction and resulting in a novel 5 amino acid change (ASCSV) SEQ ID NO:28.
- 35. (original) iPLA<sub>2</sub> $\gamma$  exons designated exons 1 (SEQ ID NO:29) and 4 (SEQ ID NO:30) corresponding to genomic sequence 135327-135622 and 125460-125571 of GenBank genomic clone RG054D04.
- 36. (original) A truncated iPLA<sub>2</sub> $\gamma$  63kDa (SEQ ID NO: 21) resulting from initiation at methionine number 122 of iPLA<sub>2</sub> $\gamma$  which is expressed in the baculoviral and in vitro expression systems at least 20 fold greater (at the mRNA and protein levels) than the full length 88kDa (SEQ ID NO: 1) protein product.
- 37. (original) A transgenic construct containing the  $\gamma$  MHC promoter upstream of the full-length iPLA<sub>2</sub> $\gamma$  coding sequence (SEQ ID NO: 6) for myocardial specific expression of recombinant iPLA<sub>2</sub> $\gamma$  in TGiPLA<sub>2</sub> $\gamma$  mice.
- 38. (original) A transgenic mouse (TGiPLA<sub>2</sub> $\gamma$ )which expresses 77kDa, 74kDa, 63kDa, and 45kDa isoforms of recombinant human iPLA<sub>2</sub> $\gamma$ .
- 39. (original) A polypeptide (SEQ ID NO: 1) with alternative ATG start sites encoding 88, 77, 74, and 63kDa iPLA<sub>2</sub>γ proteins

- 40. (original) An in vitro expression construct in which truncated iPLA<sub>2</sub> $\gamma$  sequences (SEQ ID NO: 6, 15, 18, and 21) are cloned downstream from the SV40 promoter of vector pEF.
- 41. (original) A transcription factor binding region defined by gel shift analysis between nucleotide residues 6-50 encoding the 88 kDa protein and including the sequence 5'-TATTAATCTGACTGTAGATATATATATTTACCTCCTTAGTAATGC-3' (SEQ ID NO:59) within the N-terminal coding region of iPLA<sub>2</sub>γ.
- 42. (original) Three MyoD transcription factor binding sites (E-boxes) defined by the consensus nucleotide sequence CANNTG in promoter 1 (pre exon 1) sequence of the iPLA<sub>2</sub>γ gene corresponding to nucleotide residues -22 thought -27 corresponding to nucleotide sequence 5'-CAAGTG-3' (SEQ ID NO: 60), -53 through -58 corresponding to nucleotide sequence 5'-CAGGTG-3' (SEQ ID NO:61), and -349 through -354 corresponding to nucleotide sequence 5'-CAGGTG-3' (SEQ ID NO:62) upstream from start of exon 1.
- 43. (original) An initiator (Inr) sequence with a consensus sequence of Py-Py-A-N-T/A-Py-Py at which nuclear protein constituents bind to 5'-GCG TCA CTT CCG CTG GGG GCG G-3' (SEQ ID NO: 77) at nucleotide residues -54 through -75 upstream from the putative start of exon 2.
- 44. (original) A pre exon 2 sequence 5'-GCCAGTGTTTG-3' (SEQ ID NO: 78) which is consistent with a CORE promoter element was identified in comparisons of human, mouse, and rat sequence.
- 45. (original) A transcriptional regulatory domain within the 5' coding region (nucleotide residues 1-315)(SEQ ID NO: 57) of iPLA<sub>2</sub> $\gamma$ .
- 46. (original) A nuclear binding domain corresponding to SEQ ID NO:59 defined by gel shift analysis within the transcriptional regulatory domain.
- 47. (original) iPLA<sub>2</sub> $\gamma$  exons SEQ ID NO:29 and 30 corresponding respectively to exons 1 and 4.
- 48. (original) A novel splice variant X resulting from splicing exon 1 and truncated exon 5 sequence (SEQ ID NO:5).